



PCT

## RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/505,313

TIME: 16:01:37

Input Set : A:\SeqList-0180304.txt

Output Set: N:\CRF4\08262004\J505313.raw

3 <110> APPLICANT: F. Hoffmann-La Roche AG  
 4 MorphoSys AG  
 6 <120> TITLE OF INVENTION: Anti A-beta antibodies and their use  
 8 <130> FILE REFERENCE: F 2842 PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/505,313  
 C--> 11 <141> CURRENT FILING DATE: 2004-08-20  
 13 <150> PRIOR APPLICATION NUMBER: EP 02003844.4  
 14 <151> PRIOR FILING DATE: 2002-02-20  
 16 <160> NUMBER OF SEQ ID NOS: 414  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 9  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: artificial sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: synthetic construct; first region of beta-A4 peptide  
 28 <400> SEQUENCE: 1  
 30 Ala Glu Phe Arg His Asp Ser Gly Tyr  
 31 1 5  
 34 <210> SEQ ID NO: 2  
 35 <211> LENGTH: 14  
 36 <212> TYPE: PRT  
 37 <213> ORGANISM: artificial sequence  
 39 <220> FEATURE:  
 40 <223> OTHER INFORMATION: synthetic construct; second region of beta-A4 peptide  
 42 <400> SEQUENCE: 2  
 44 Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly  
 45 1 5 10  
 48 <210> SEQ ID NO: 3  
 49 <211> LENGTH: 368  
 50 <212> TYPE: DNA  
 51 <213> ORGANISM: artificial sequence  
 53 <220> FEATURE:  
 54 <223> OTHER INFORMATION: synthetic construct; VH-region of MS-Roche#3  
 56 <400> SEQUENCE: 3  
 57 caggtgcaat tgggtggaag cggcgggcgc ctggtgcaac cggcgggcag cctgcgtctg 60  
 59 agctgcgcgg cctccggatt taccttttagc agctatgcga tgagctgggt gcgccaagcc 120  
 61 cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180  
 63 gcggatagcg tgaaaggccg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240  
 65 ctgcaaatac acagcctgcg tgcggaagat acggcctgtg attattgcgc gcgtcttact 300  
 67 cattatgctc gttattatcg ttattttgat gtttggggcc aaggcaccct ggtgacggtt 360  
 69 agctcagc 368  
 72 <210> SEQ ID NO: 4



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Input Set : A:\SeqList-0180304.txt

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73 &lt;211&gt; LENGTH: 122

74 &lt;212&gt; TYPE: PRT

75 &lt;213&gt; ORGANISM: artificial sequence

77 &lt;220&gt; FEATURE:

78 &lt;223&gt; OTHER INFORMATION: synthetic construct; VH-region of MS-Roche#3

80 &lt;400&gt; SEQUENCE: 4

82 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

83 1 5 10 15

86 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

87 20 25 30

90 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

91 35 40 45

94 Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val

95 50 55 60

98 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

99 65 70 75 80

102 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

103 85 90 95

106 Ala Arg Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp

107 100 105 110

110 Gly Gln Gly Thr Leu Val Thr Val Ser Ser

111 115 120

114 &lt;210&gt; SEQ ID NO: 5

115 &lt;211&gt; LENGTH: 379

116 &lt;212&gt; TYPE: DNA

117 &lt;213&gt; ORGANISM: artificial sequence

119 &lt;220&gt; FEATURE:

120 &lt;223&gt; OTHER INFORMATION: synthetic construct; VH-region of MS-Roche#7

122 &lt;400&gt; SEQUENCE: 5

123 caggtgcaat tgggtgaaag cggcgggcggc ctggtgcaac cggcgggcag cctgcgtctg 60

125 agctgcgcgg cctccggatt taccttttagc agctatgcga tgagctgggt gcgccaagcc 120

127 cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180

129 gcggatagcg tgaaaggccg tttaccattt cacgtgataa ttcgaaaaac accctgtatc 240

131 tgcaaatgaa cagcctgcgt gcggaagata cggccgtgta ttattgcgcg cgtggtaagg 300

133 gtaataactca taagccttat gggtatgttc gttattttga tgtttggggc caaggcaccc 360

135 tgggtgacggt tagctcagc 379

138 &lt;210&gt; SEQ ID NO: 6

139 &lt;211&gt; LENGTH: 126

140 &lt;212&gt; TYPE: PRT

141 &lt;213&gt; ORGANISM: artificial sequence

143 &lt;220&gt; FEATURE:

144 &lt;223&gt; OTHER INFORMATION: synthetic construct; VH-region of MS-Roche#7

146 &lt;400&gt; SEQUENCE: 6

148 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

149 1 5 10 15

152 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

153 20 25 30

156 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

157 35 40 45

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160 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
161      50                      55                      60
164 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
165 65                      70                      75                      80
168 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
169                      85                      90                      95
172 Ala Arg Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr
173                      100                      105                      110
176 Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
177      115                      120                      125
180 <210> SEQ ID NO: 7
181 <211> LENGTH: 374
182 <212> TYPE: DNA
183 <213> ORGANISM: artificial sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: synthetic construct; VH-region of MS-Roche#8
188 <400> SEQUENCE: 7
189 caggtgcaat tgggtggaag cggcgggcggc ctggtgcaac cgggcggcag cctgcgtctg      60
191 agctgcgcgg cctccggatt taccttttagc agctatgcga tgagctgggt gcgccaagcc      120
193 cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat      180
195 gcggatagcg tgaaaggccg ttttaccatt tcacgtgata attcgaaaaa caccctgtat      240
197 ctgcaaataga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgtcttctt      300
199 tctcgtgggtt ataatggtta ttatcataag tttgatgttt ggggccaagg caccctgggtg      360
201 acggttagct cagc                                     374
204 <210> SEQ ID NO: 8
205 <211> LENGTH: 124
206 <212> TYPE: PRT
207 <213> ORGANISM: artificial sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: synthetic construct; VH-region of MS-Roche#8
212 <400> SEQUENCE: 8
214 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
215 1                      5                      10                      15
218 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
219      20                      25                      30
222 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
223      35                      40                      45
226 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
227      50                      55                      60
230 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
231 65                      70                      75                      80
234 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
235      85                      90                      95
238 Ala Arg Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp
239      100                      105                      110
242 Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
243      115                      120
246 <210> SEQ ID NO: 9
247 <211> LENGTH: 330

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248 <212> TYPE: DNA
249 <213> ORGANISM: artificial sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: synthetic construct; VL-region of MS-Roche#3
254 <400> SEQUENCE: 9
255 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc      60
257 ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa      120
259 ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tgggggtcccg      180
261 gcgcgtttta gcggtctctg atccggcacg gattttaccc tgaccattag cagcctggaa      240
263 cctgaagact ttgcggttta ttattgccag caggtttata atcctcctgt tacctttggc      300
265 cagggtacga aagttgaaat taaacgtacg                                     330
268 <210> SEQ ID NO: 10
269 <211> LENGTH: 110
270 <212> TYPE: PRT
271 <213> ORGANISM: artificial sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: synthetic construct; VL-region of MS-Roche#3
276 <400> SEQUENCE: 10
278 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
279 1           5           10          15
282 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
283           20          25          30
286 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
287           35          40          45
290 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
291           50          55          60
294 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
295 65           70          75          80
298 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Val Tyr Asn Pro Pro
299           85          90          95
302 Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
303           100         105         110
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 330
308 <212> TYPE: DNA
309 <213> ORGANISM: artificial sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: synthetic construct; VL-region of MS-Roche#7
314 <400> SEQUENCE: 11
315 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc      60
317 ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa      120
319 ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tgggggtcccg      180
321 gcgcgtttta gcggtctctg atccggcacg gattttaccc tgaccattag cagcctggaa      240
323 cctgaagact ttgcgactta ttattgcttt cagctttatt ctgatccttt tacctttggc      300
325 cagggtacga aagttgaaat taaacgtacg                                     330
328 <210> SEQ ID NO: 12
329 <211> LENGTH: 110
330 <212> TYPE: PRT
331 <213> ORGANISM: artificial sequence

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333 &lt;220&gt; FEATURE:

334 &lt;223&gt; OTHER INFORMATION: synthetic construct; VL-region of MS-Roche#7

336 &lt;400&gt; SEQUENCE: 12

338 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

339 1 5 10 15

342 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

343 20 25 30

346 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

347 35 40 45

350 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser

351 50 55 60

354 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu

355 65 70 75 80

358 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Leu Tyr Ser Asp Pro

359 85 90 95

362 Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr

363 100 105 110

366 &lt;210&gt; SEQ ID NO: 13

367 &lt;211&gt; LENGTH: 330

368 &lt;212&gt; TYPE: DNA

369 &lt;213&gt; ORGANISM: artificial sequence

371 &lt;220&gt; FEATURE:

372 &lt;223&gt; OTHER INFORMATION: synthetic construct; VL-region of MS-Roche#8

374 &lt;400&gt; SEQUENCE: 13

375 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgagacc 60

377 ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

379 ccaggtcaag caccgcgtct attaatatattat ggcgcgagca gccgtgcaac tgggggtccc 180

381 gcgcgtttta gcggtctctg atccggcacg gattttaccc tgaccattag cagcctggaa 240

383 cctgaagact ttgcgactta ttattgccag cagctttctt cttttctctc tacctttggc 300

385 cagggtacga aagttgaaat taaacgtacg 330

388 &lt;210&gt; SEQ ID NO: 14

389 &lt;211&gt; LENGTH: 110

390 &lt;212&gt; TYPE: PRT

391 &lt;213&gt; ORGANISM: artificial sequence

393 &lt;220&gt; FEATURE:

394 &lt;223&gt; OTHER INFORMATION: synthetic construct; VL-region of MS-Roche#8

396 &lt;400&gt; SEQUENCE: 14

398 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

399 1 5 10 15

402 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

403 20 25 30

406 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

407 35 40 45

410 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser

411 50 55 60

414 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu

415 65 70 75 80

418 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Ser Ser Phe Pro

419 85 90 95

**RAW SEQUENCE LISTING ERROR SUMMARY**  
**PATENT APPLICATION: US/10/505,313**DATE: 08/26/2004  
TIME: 16:01:38Input Set : A:\SeqList-0180304.txt  
Output Set : N:\CRF4\08262004\J505313.raw**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:225; Xaa Pos. 85,89,91,92,93,94,95,96  
Seq#:226; Xaa Pos. 94,96,97,98,99,100,101  
Seq#:227; Xaa Pos. 86,90,92,93,94,95,96,97  
Seq#:228; Xaa Pos. 95,97,98,99,100,101,102  
Seq#:229; Xaa Pos. 92,94,95,96,97,98,99  
Seq#:230; Xaa Pos. 93,95,96,97,98,99,100  
Seq#:231; Xaa Pos. 90,92,93,94,95,96,97  
Seq#:232; Xaa Pos. 99,100,101,102,103,104,105,106,107,108,109,110,111,112  
Seq#:232; Xaa Pos. 113,114,116  
Seq#:233; Xaa Pos. 99,100,101,102,103,104,105,106,107,108,109,110,111,112  
Seq#:233; Xaa Pos. 113,114,116  
Seq#:234; Xaa Pos. 100,101,102,103,104,105,106,107,108,109,110,111,112,113  
Seq#:234; Xaa Pos. 114,115,117  
Seq#:235; Xaa Pos. 99,100,101,102,103,104,105,106,107,108,109,110,111,112  
Seq#:235; Xaa Pos. 113,114,116  
Seq#:236; Xaa Pos. 98,99,100,101,102,103,104,105,106,107,108,109,110,111  
Seq#:236; Xaa Pos. 112,113,115  
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Seq#:238; Xaa Pos. 102,103,104,105,106,107,108,109,110,111,112,113,114,115  
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Seq#:239; N Pos. 253,254,255,265,266,267,271,272,273,274,275,276,277,278  
Seq#:239; N Pos. 279,280,281,282,283,284,285,286,287,288  
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Seq#:242; N Pos. 283,284,285,289,290,291,292,293,294,295,296,297,298,299  
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Seq#:244; N Pos. 291,292,293,294,295,296,297  
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Seq#:248; N Pos. 298,299,300,301,302,303,304,305,306,307,308,309,310,311  
Seq#:248; N Pos. 312,313,314,315,316,317,318,319,320,321,322,323,324,325  
Seq#:248; N Pos. 326,327,328,329,330,331,332,333,334,335,336,337,338,339

**RAW SEQUENCE LISTING ERROR SUMMARY**  
**PATENT APPLICATION: US/10/505,313**

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Input Set : A:\SeqList-0180304.txt

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Seq#:248; N Pos. 340,341,342,343,344,345,349,350,351  
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 Seq#:250; N Pos. 292,293,294,295,296,297,298,299,300,301,302,303,304,305  
 Seq#:250; N Pos. 306,307,311  
 Seq#:251; N Pos. 295,296,297,298,299,300,301,302,303,304,305,306,307,308  
 Seq#:251; N Pos. 309,310,314

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/505,313

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Input Set : A:\SeqList-0180304.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:4247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:225 after pos.:80  
L:4334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:226 after pos.:80  
M:341 Repeated in SeqNo=226  
L:4431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:227 after pos.:80  
M:341 Repeated in SeqNo=227  
L:4518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:228 after pos.:80  
M:341 Repeated in SeqNo=228  
L:4584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:229 after pos.:80  
M:341 Repeated in SeqNo=229  
L:4646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:230 after pos.:80  
M:341 Repeated in SeqNo=230  
L:4708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:231 after pos.:80  
M:341 Repeated in SeqNo=231  
L:4776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:232 after pos.:96  
M:341 Repeated in SeqNo=232  
L:4844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:233 after pos.:96  
M:341 Repeated in SeqNo=233  
L:4912 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:234 after pos.:96  
M:341 Repeated in SeqNo=234  
L:4980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:235 after pos.:96  
M:341 Repeated in SeqNo=235  
L:5048 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:236 after pos.:96  
M:341 Repeated in SeqNo=236  
L:5116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:237 after pos.:96  
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L:5184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:238 after pos.:96  
M:341 Repeated in SeqNo=238  
L:5264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:239 after pos.:240  
L:5331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:240 after pos.:240  
L:5404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:241 after pos.:240  
L:5471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242 after pos.:240  
M:341 Repeated in SeqNo=242  
L:5520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:243 after pos.:240  
L:5569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:244 after pos.:240  
L:5618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:245 after pos.:240  
L:5667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:246 after pos.:240  
M:341 Repeated in SeqNo=246  
L:5718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:247 after pos.:240  
M:341 Repeated in SeqNo=247  
L:5769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:248 after pos.:240  
M:341 Repeated in SeqNo=248  
L:5820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:249 after pos.:240  
M:341 Repeated in SeqNo=249  
L:5869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:250 after pos.:240  
M:341 Repeated in SeqNo=250  
L:5918 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:251 after pos.:240



**VERIFICATION SUMMARY**

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Input Set : A:\SeqList-0180304.txt

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M:341 Repeated in SeqNo=251

L:5969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:252 after pos.:300